

Preprocessing

```
In [1]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

%matplotlib inline
```

```
In [2]: liver_df = pd.read_csv('liverLabTrain.csv')
```

```
In [3]: liver_df.head(10)
```

Out[3]:

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Aminotransferase
0	65	Female	0.7	0.1	187	16
1	62	Male	10.9	5.5	699	64
2	62	Male	7.3	4.1	490	60
3	58	Male	1.0	0.4	182	14
4	72	Male	3.9	2.0	195	27
5	46	Male	1.8	0.7	208	19
6	26	Female	0.9	0.2	154	16
7	29	Female	0.9	0.3	202	14
8	51	Male	2.9	1.3	482	22
9	62	Male	6.8	3.0	542	116

```
In [4]: from sklearn.preprocessing import OneHotEncoder
```

Binarizing the gender column

```
In [5]: for i,x in enumerate(liver_df['Gender']):
        if x.lower() == 'female':
            liver_df['Gender'].iloc[i] = 0
        else:
            liver_df['Gender'].iloc[i] = 1
```

c:\program files\python37\lib\site-packages\pandas\core\indexing.py:670: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy (https://pandas.pydata.org/pandas-docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy)
self._setitem_with_indexer(indexer, value)

```
In [6]: liver_df.head(5)
```

Out[6]:

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Aminotransferase
0	65	0	0.7	0.1	187	16
1	62	1	10.9	5.5	699	64
2	62	1	7.3	4.1	490	60
3	58	1	1.0	0.4	182	14
4	72	1	3.9	2.0	195	27

In [7]: `liver_df.info()`

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 483 entries, 0 to 482
Data columns (total 11 columns):
#   Column                                Non-Null Count  Dtype
---  -
0   Age                                   483 non-null    int64
1   Gender                               483 non-null    object
2   Total_Bilirubin                      483 non-null    float64
3   Direct_Bilirubin                    483 non-null    float64
4   Alkaline_Phosphotase                 483 non-null    int64
5   Alamine_Aminotransferase             483 non-null    int64
6   Aspartate_Aminotransferase           483 non-null    int64
7   Total_Protiens                      483 non-null    float64
8   Albumin                             483 non-null    float64
9   Albumin_and_Globulin_Ratio           480 non-null    float64
10  Liver_Disease                        483 non-null    int64
dtypes: float64(5), int64(5), object(1)
memory usage: 41.6+ KB
```

In [8]: `liver_df.describe()`

Out[8]:

	Age	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Aminotransferase
count	483.000000	483.000000	483.000000	483.000000	483.000000
mean	44.722567	3.299172	1.466253	287.335404	72.111801
std	16.263700	6.358002	2.783368	232.322630	148.754051
min	4.000000	0.400000	0.100000	75.000000	10.000000
25%	33.000000	0.800000	0.200000	174.500000	23.000000
50%	45.000000	1.000000	0.300000	206.000000	34.000000
75%	57.000000	2.600000	1.250000	298.000000	58.000000
max	90.000000	75.000000	19.700000	2110.000000	1680.000000

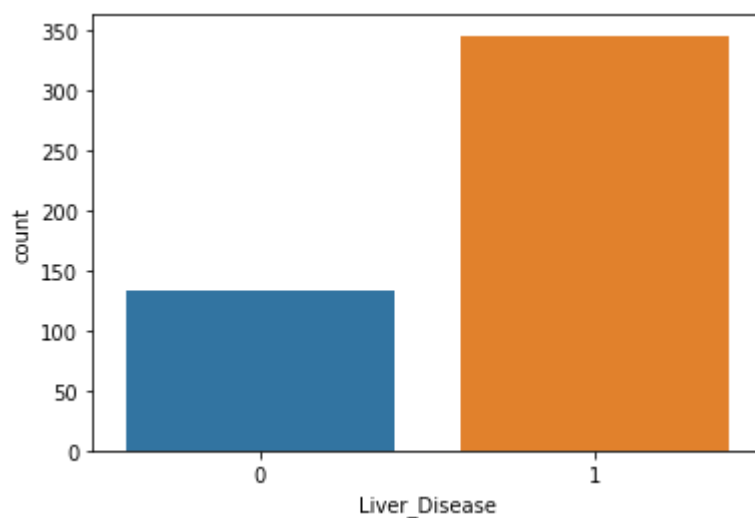
Missing data

In [9]: `liver_df.dropna(inplace=True) #Dropping 3 rows where Albumin_and_Globulin_Ratio is`

Visualizations

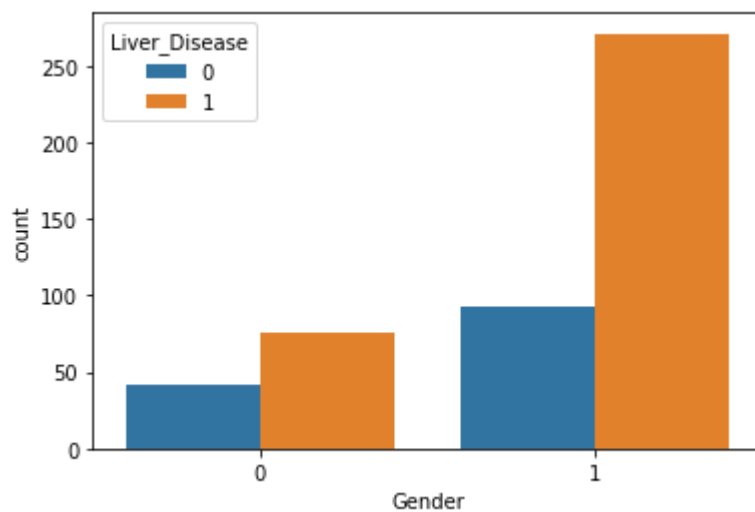
```
In [10]: sns.countplot(liver_df['Liver_Disease'])
```

```
Out[10]: <matplotlib.axes._subplots.AxesSubplot at 0x1c2757752c8>
```



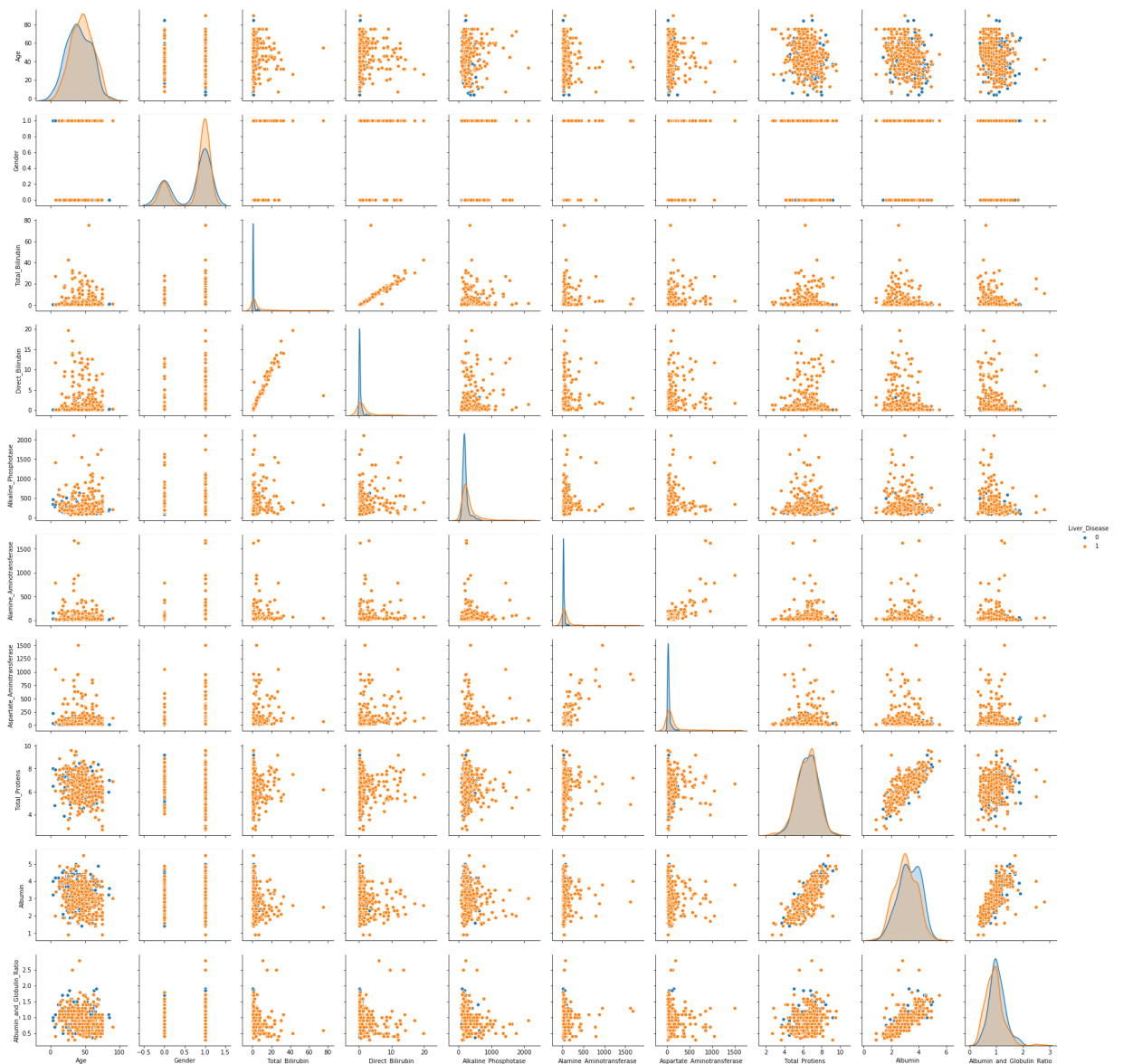
```
In [11]: sns.countplot(data = liver_df, x = 'Gender', hue='Liver_Disease')
```

```
Out[11]: <matplotlib.axes._subplots.AxesSubplot at 0x1c2787d6808>
```



```
In [12]: sns.pairplot(data = liver_df, hue = 'Liver_Disease')
```

```
Out[12]: <seaborn.axisgrid.PairGrid at 0x1c27888fe48>
```



Preparing data for model

```
In [13]: X = liver_df.drop(['Liver_Disease'], axis = 1)
```

```
In [14]: y = liver_df['Liver_Disease']
```

In [15]: X

Out[15]:

	Age	Gender	Total_Bilirubin	Direct_Bilirubin	Alkaline_Phosphotase	Alamine_Aminotransferase
0	65	0	0.7	0.1	187	16
1	62	1	10.9	5.5	699	64
2	62	1	7.3	4.1	490	60
3	58	1	1.0	0.4	182	14
4	72	1	3.9	2.0	195	21
...
478	60	1	0.5	0.1	500	20
479	40	1	0.6	0.1	98	35
480	52	1	0.8	0.2	245	48
481	31	1	1.3	0.5	184	29
482	38	1	1.0	0.3	216	21

480 rows × 10 columns

In [16]: y

Out[16]:

```
0      1
1      1
2      1
3      1
4      1
..
478    0
479    1
480    1
481    1
482    0
```

Name: Liver_Disease, Length: 480, dtype: int64

In [17]: `from sklearn.model_selection import train_test_split`In [18]: `X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_s`

Oversampling

In [19]: `#https://beckernick.github.io/oversampling-modeling/`

```
In [20]: from imblearn.over_sampling import SMOTE
```

Using TensorFlow backend.

```
c:\program files\python37\lib\site-packages\tensorflow\python\framework\dtypes.py:526: FutureWarning: Passing (type, 1) or '1type' as a synonym of type is deprecated; in a future version of numpy, it will be understood as (type, (1,)) / '(1,)type'.
```

```
_np_qint8 = np.dtype [("qint8", np.int8, 1)]
```

```
c:\program files\python37\lib\site-packages\tensorflow\python\framework\dtypes.py:527: FutureWarning: Passing (type, 1) or '1type' as a synonym of type is deprecated; in a future version of numpy, it will be understood as (type, (1,)) / '(1,)type'.
```

```
_np_quint8 = np.dtype [("quint8", np.uint8, 1)]
```

```
c:\program files\python37\lib\site-packages\tensorflow\python\framework\dtypes.py:528: FutureWarning: Passing (type, 1) or '1type' as a synonym of type is deprecated; in a future version of numpy, it will be understood as (type, (1,)) / '(1,)type'.
```

```
_np_qint16 = np.dtype [("qint16", np.int16, 1)]
```

```
c:\program files\python37\lib\site-packages\tensorflow\python\framework\dtypes.py:529: FutureWarning: Passing (type, 1) or '1type' as a synonym of type is deprecated; in a future version of numpy, it will be understood as (type, (1,)) / '(1,)type'.
```

```
_np_quint16 = np.dtype [("quint16", np.uint16, 1)]
```

```
c:\program files\python37\lib\site-packages\tensorflow\python\framework\dtypes.py:530: FutureWarning: Passing (type, 1) or '1type' as a synonym of type is deprecated; in a future version of numpy, it will be understood as (type, (1,)) / '(1,)type'.
```

```
_np_qint32 = np.dtype [("qint32", np.int32, 1)]
```

```
c:\program files\python37\lib\site-packages\tensorflow\python\framework\dtypes.py:535: FutureWarning: Passing (type, 1) or '1type' as a synonym of type is deprecated; in a future version of numpy, it will be understood as (type, (1,)) / '(1,)type'.
```

```
np_resource = np.dtype [("resource", np.ubyte, 1)]
```

```
In [22]: sm = SMOTE(random_state=42)
x_train_res, y_train_res = sm.fit_sample(X_train, y_train)
```

Using GridSearchCV to find the best parameters for Logistic Regression

```
In [23]: from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import GridSearchCV
from sklearn.ensemble import RandomForestClassifier
```

```
In [24]: estimators = [20, 40, 60, 80, 100]
criterion = ['gini', 'entropy']
min_samples_split = [2,3,4]
max_features = ['auto', 'sqrt']
```

```
# Create hyperparameter options
```

```
hyperparameters = dict(n_estimators=estimators,criterion = criterion,min_samples_
```

```
In [25]: rf = RandomForestClassifier(verbose=1, random_state=42)
```

```
In [26]: clf = GridSearchCV(rf, hyperparameters, cv=5, verbose=0)
```

```
In [27]: best_model = clf.fit(X_train, y_train)
```

```
[Parallel(n_jobs=1)]: Done 20 out of 20 | elapsed: 0.0s finished
[Parallel(n_jobs=1)]: Using backend SequentialBackend with 1 concurrent worke
rs.
[Parallel(n_jobs=1)]: Done 20 out of 20 | elapsed: 0.0s finished
[Parallel(n_jobs=1)]: Using backend SequentialBackend with 1 concurrent worke
rs.
[Parallel(n_jobs=1)]: Done 20 out of 20 | elapsed: 0.0s finished
[Parallel(n_jobs=1)]: Using backend SequentialBackend with 1 concurrent worke
rs.
[Parallel(n_jobs=1)]: Done 40 out of 40 | elapsed: 0.0s finished
[Parallel(n_jobs=1)]: Using backend SequentialBackend with 1 concurrent worke
rs.
[Parallel(n_jobs=1)]: Done 40 out of 40 | elapsed: 0.0s finished
[Parallel(n_jobs=1)]: Using backend SequentialBackend with 1 concurrent worke
rs.
[Parallel(n_jobs=1)]: Done 40 out of 40 | elapsed: 0.0s finished
[Parallel(n_jobs=1)]: Using backend SequentialBackend with 1 concurrent worke
rs.
[Parallel(n_jobs=1)]: Done 40 out of 40 | elapsed: 0.0s finished
```

```
In [28]: print('Best n_estimators:', best_model.best_estimator_.get_params()['n_estimators'])
print('Best criterion:', best_model.best_estimator_.get_params()['criterion'])
print('Best max_features:', best_model.best_estimator_.get_params()['max_features'])
print('Best min_samples_split:', best_model.best_estimator_.get_params()['min_san
```

```
Best n_estimators: 20
Best criterion: entropy
Best max_features: auto
Best min_samples_split: 3
```

Training with the best parameters


```
In [29]: tuned_rf = RandomForestClassifier(n_estimators=20,
                                         criterion='entropy',
                                         max_features='auto',
                                         min_samples_split=3)
```

```
In [30]: tuned_rf.fit(X_train,y_train)
```

```
Out[30]: RandomForestClassifier(bootstrap=True, ccp_alpha=0.0, class_weight=None,
                               criterion='entropy', max_depth=None, max_features='auto',
                               max_leaf_nodes=None, max_samples=None,
                               min_impurity_decrease=0.0, min_impurity_split=None,
                               min_samples_leaf=1, min_samples_split=3,
                               min_weight_fraction_leaf=0.0, n_estimators=20,
                               n_jobs=None, oob_score=False, random_state=None,
                               verbose=0, warm_start=False)
```

```
In [31]: y_preds = tuned_rf.predict(X_test)
```

```
In [32]: from sklearn.metrics import classification_report
```

```
In [33]: print(classification_report(y_test,y_preds))
```

	precision	recall	f1-score	support
0	0.58	0.48	0.53	29
1	0.79	0.85	0.82	67
accuracy			0.74	96
macro avg	0.69	0.67	0.67	96
weighted avg	0.73	0.74	0.73	96

```
In [ ]:
```